

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A primer which ~~specifically~~ amplifies *groEL2* gene fragment of at least one *Streptomyces* species ~~comprising~~ consisting of the nucleotide sequence of SEQ ID NO: 1.
2. (Currently Amended) A primer which ~~specifically~~ amplifies *groEL2* gene fragment of at least one *Streptomyces* species ~~comprising~~ consisting of the nucleotide sequence of SEQ ID NO: 2 and optionally additional nucleotide sequences comprising the complement of adjacent nucleotide sequences of *S. lividans* (GenBank No. X95971), *S. albus* (GenBank No. M76658), and *T. paurometabola* (GenBank No. AF352578).
3. (Withdrawn) A *groEL2* gene fragment derived from *Streptomyces* species or fragment thereof comprising a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.
4. (Currently Amended) ~~[[A]]~~ An isolated *groEL2* gene fragment derived from a potato scab pathogenic microorganism ~~or fragment thereof comprising a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61~~ SEQ ID NO: 43.
5. (Withdrawn) A method for identifying *Streptomyces* species comprising:
 - a) amplifying *groEL2* gene fragment of target strain using a primer which is capable of specifically amplifying *groEL2* gene of *Streptomyces* species;

b) analyzing the nucleotide sequence of *groEL2* gene fragment thus amplified;
and

c) comparing the nucleotide sequence obtained in b) with that of *groEL2* gene fragment of a reference strain.

6. (Withdrawn) The method of claim 5, wherein the primer is chosen from at least one of

a) a primer comprising the nucleotide sequence of SEQ ID NO: 1 and

b) a primer comprising the nucleotide sequence of SEQ ID NO: 2.

7. (Withdrawn) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

8. (Withdrawn) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.

9. (Withdrawn) The method of claim 5, wherein c) further comprises multi-aligning the nucleotide sequences and forming a phylogenetic tree.

10. (New) A primer which specifically amplifies *groEL2* gene fragment of *Streptomyces* species consisting of the nucleotide sequence of SEQ ID NO: 2.

11. (New) The *groEL2* gene fragment of claim 4, wherein the fragment is 420 or 423 nucleotides long.

12. (New) The *groEL2* gene fragment of claim 4, wherein the fragment is SEQ ID NO: 43.

13. (New) An isolated *groEL2* gene fragment derived from a potato scab pathogenic microorganism comprising a polynucleotide chosen from the nucleotide sequences of any one of SEQ ID NOs: 44 to 61.

14. (New) An isolated *groEL2* gene fragment produced by amplification from a potato scab pathogenic microorganism using

- a) a primer consisting of the nucleotide sequence of SEQ ID NO: 1 and
- b) a primer consisting of the nucleotide sequence of SEQ ID NO: 2.